



09/762045 #3

## SEQUENCE LISTING

<110> Reindl, Andreas  
Mejia, Patricia Leon  
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Gracia, Maria Araceli Cantero  
Ebneth, Marcus  
Herbers, Karin

<120> DNA sequence coding for a 1-deoxy-D-xylulose-5-phosphate synthase and overproduction thereof in plants

<130> 0817/000006/MEC

<140> US 09/762,045  
<141> 2001-02-01

<150> PCT/EP99/05467  
<151> 1999-07-30

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<170> PatentIn Vers. 2.0/WordPerfect 6.0

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585

590

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 370 375 380

Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr  
 385 390 395 400

Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe  
 405 410 415

Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln  
 420 425 430

Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile  
 435 440 445

Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly  
 450 455 460

Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn  
 465 470 475 480

Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys  
 485 490 495

Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly  
 500 505 510

Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr  
 515 520 525

Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu

530 535 540

Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala  
545 550 555 560

Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His  
565 570 575

Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile  
580 585 590

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<212> DNA

<213> Streptomyces avermitilis

<220>

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gagcactccg atgcgcggct cccgcgcag cagcaccagg agccggccgt ccagatgatc 180

gatcgccacg gcagccctc cagtggtcat cctgtac atg cag ccc cac gcc atg 235  
Met Gln Pro His Ala Met  
1 5

ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca 283  
Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala  
10 15 20

cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca 331  
Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro  
25 30 35

cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat 379  
His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn  
40 45 50

gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta 427  
Gly Arg Gly Arg Leu Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu  
55 60 65 70

ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa 475  
Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu  
75 80 85

cg<sub>g</sub> c<sub>g</sub> c<sub>g</sub> c<sub>g</sub> c<sub>g</sub> a<sub>c</sub> c<sub>g</sub> t<sub>tc</sub> g<sub>ta</sub> c<sub>gt</sub> c<sub>c</sub>t c<sub>a</sub>c c<sub>aa</sub> c<sub>g</sub>g c<sub>tc</sub> g<sub>gc</sub> a<sub>cg</sub> 523  
 Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr  
 90 95 100

c<sub>tt</sub> c<sub>gt</sub> c<sub>ct</sub> c<sub>ac</sub> c<sub>tc</sub> c<sub>gt</sub> c<sub>at</sub> c<sub>aa</sub> g<sub>cc</sub> c<sub>gc</sub> c<sub>ac</sub> c<sub>cc</sub> c<sub>tg</sub> g<sub>gg</sub> c<sub>ca</sub> c<sub>tt</sub> 571  
 Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu  
 105 110 115

c<sub>ct</sub> c<sub>gc</sub> c<sub>g</sub>a c<sub>ca</sub> t<sub>gt</sub> g<sub>gc</sub> c<sub>g</sub>a g<sub>ca</sub> c<sub>gg</sub> c<sub>g</sub>a c<sub>gt</sub> c<sub>gt</sub> c<sub>g</sub>a c<sub>ct</sub> c<sub>gc</sub> 619  
 Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Pro Arg  
 120 125 130

c<sub>at</sub> c<sub>g</sub>a g<sub>gt</sub> c<sub>cc</sub> g<sub>ga</sub> c<sub>g</sub>c c<sub>cg</sub> c<sub>g</sub>c c<sub>ca</sub> c<sub>g</sub>c g<sub>ta</sub> c<sub>g</sub>c g<sub>at</sub> c<sub>g</sub>a g<sub>ca</sub> 667  
 His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala  
 135 140 145 150

c<sub>g</sub>g c<sub>g</sub>c c<sub>g</sub> c<sub>tc</sub> g<sub>gt</sub> c<sub>g</sub>c c<sub>g</sub>a g<sub>cc</sub> g<sub>ta</sub> c<sub>g</sub>a g<sub>ct</sub> g<sub>aa</sub> g<sub>ga</sub> c<sub>g</sub>a g<sub>ca</sub> c<sub>gg</sub> 715  
 Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg  
 155 160 165

c<sub>ac</sub> g<sub>gt</sub> c<sub>gt</sub> c<sub>ct</sub> c<sub>gc</sub> c<sub>g</sub>c g<sub>at</sub> c<sub>g</sub>c c<sub>ac</sub> c<sub>ta</sub> c<sub>gg</sub> c<sub>aa</sub> g<sub>ac</sub> c<sub>cg</sub> c<sub>ca</sub> c<sub>ac</sub> 763  
 His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His  
 170 175 180

c<sub>ct</sub> c<sub>gt</sub> c<sub>g</sub>a c<sub>cg</sub> g<sub>ac</sub> c<sub>gg</sub> c<sub>ta</sub> c<sub>g</sub>a c<sub>gg</sub> c<sub>cc</sub> c<sub>ta</sub> c<sub>ct</sub> c<sub>cc</sub> c<sub>gg</sub> c<sub>ta</sub> c<sub>gt</sub> 811  
 Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg  
 185 190 195

g<sub>gc</sub> c<sub>g</sub>c c<sub>g</sub>c c<sub>cc</sub> g<sub>at</sub> c<sub>gt</sub> c<sub>g</sub>a a<sub>cc</sub> g<sub>cc</sub> c<sub>g</sub>c c<sub>ca</sub> c<sub>cg</sub> c<sub>ac</sub> c<sub>tt</sub> c<sub>ca</sub> g<sub>gc</sub> 859  
 Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly  
 200 205 210

c<sub>at</sub> c<sub>g</sub>a c<sub>ca</sub> c<sub>tg</sub> c<sub>gt</sub> c<sub>gg</sub> c<sub>aa</sub> c<sub>gt</sub> c<sub>g</sub>a g<sub>ct</sub> c<sub>gg</sub> c<sub>cg</sub> g<sub>at</sub> g<sub>aa</sub> c<sub>g</sub>a a<sub>tg</sub> 907  
 His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met  
 215 220 225 230

g<sub>gt</sub> c<sub>gg</sub> c<sub>tt</sub> c<sub>ta</sub> c<sub>aa</sub> c<sub>aa</sub> g<sub>gt</sub> c<sub>at</sub> g<sub>gg</sub> c<sub>tt</sub> c<sub>ac</sub> g<sub>aa</sub> c<sub>at</sub> g<sub>aa</sub> g<sub>ga</sub> g<sub>tt</sub> 955  
 Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Gly Val  
 235 240 245

c<sub>gt</sub> g<sub>gg</sub> c<sub>g</sub>a c<sub>g</sub>a c<sub>at</sub> c<sub>g</sub>c g<sub>ac</sub> c<sub>g</sub>a g<sub>ta</sub> c<sub>tc</sub> g<sub>gc</sub> g<sub>ct</sub> g<sub>at</sub> g<sub>tc</sub> g<sub>aa</sub> g<sub>gt</sub> 1003  
 Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly  
 250 255 260

c<sub>gt</sub> g<sub>gc</sub> c<sub>g</sub>a c<sub>gg</sub> c<sub>ac</sub> g<sub>ct</sub> c<sub>aa</sub> g<sub>gt</sub> c<sub>aa</sub> g<sub>tt</sub> c<sub>cc</sub> g<sub>at</sub> c<sub>aa</sub> c<sub>g</sub>a g<sub>cc</sub> c<sub>gc</sub> 1051  
 Arg Gly Arg Arg His Ala Gln Gly Gln Val Pro Asp Gln Arg Ala Arg  
 265 270 275

c<sub>ct</sub> c<sub>gc</sub> c<sub>aa</sub> g<sub>aa</sub> g<sub>aa</sub> g<sub>tc</sub> c<sub>ca</sub> g<sub>at</sub> c<sub>g</sub>a c<sub>g</sub>a g<sub>ta</sub> c<sub>ct</sub> g<sub>ga</sub> g<sub>tt</sub> c<sub>ta</sub> c<sub>gg</sub> 1099  
 Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg  
 280 285 290

c<sub>gg</sub> c<sub>g</sub>c g<sub>gg</sub> c<sub>gt</sub> c<sub>ca</sub> g<sub>ca</sub> c<sub>at</sub> c<sub>g</sub>c g<sub>ct</sub> g<sub>aa</sub> c<sub>ac</sub> g<sub>gg</sub> t<sub>ga</sub> c<sub>atcg</sub>tc<sub>gag</sub> 1148  
 Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly  
 295 300

acggta<sub>cg</sub>ca c<sub>gat</sub>gc<sub>gc</sub>gc c<sub>gc</sub>cc<sub>gg</sub>cg<sub>tc</sub> c<sub>agtt</sub>c<sub>ct</sub>gg acacgccc<sub>ga</sub> c<sub>tc</sub>cg<sub>t</sub>act<sub>ac</sub> 1208  
 gacaccctcg g<sub>gg</sub>g<sub>gt</sub>gg<sub>gt</sub> g<sub>gg</sub>gc<sub>ac</sub>acc<sub>c</sub> c<sub>gc</sub>gtcccc<sub>g</sub> tc<sub>gac</sub>acc<sub>c</sub>tc<sub>g</sub>gag<sub>c</sub> 1268

aagatcctcg cggaccgcga cgaggacggc tatctgctcc agatcttac caagccggc 1328  
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 <213> Streptomyces avermitilis

<400> 6

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Gln Ala Asn Tyr Cys Ala Pro Cys Gly Thr Glu Arg Pro Cys Arg His  
 20 25 30

Asp Ala Asp His Thr Pro His Ser Arg His Arg Pro Ala Gly Arg Pro  
 35 40 45

Leu Pro Gly Glu Gly Asn Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg  
 50 55 60

Gln Ala Gly Arg Ala Leu Leu His Arg Leu Arg His Ala Ala Cys Gly  
 65 70 75 80

Val Leu Arg Thr Gly Glu Arg Gln Pro Arg Asp Arg Phe Val Arg Pro  
 85 90 95

His Gln Arg Leu Gly Thr Leu Arg Pro His Leu Arg His Gln Ala Arg  
 100 105 110

His Pro Leu Gly Pro Leu Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg  
 115 120 125

Arg Arg Arg Arg Pro Arg His Arg Gly Pro Gly Arg Pro Arg Arg Pro  
 130 135 140

Arg Val Arg Asp Arg Ala Arg Arg Pro Leu Gly Arg Arg Ala Val Arg  
 145 150 155 160

Ala Glu Gly Arg Ala Arg His Gly Arg Pro Arg Arg Asp Arg His Leu  
 165 170 175

Arg Gln Asp Pro Pro His Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro  
 180 185 190

Leu Pro Pro Arg Leu Arg Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg  
 195 200 205

Pro Pro His Leu Pro Gly His Arg Pro Leu Arg Arg Gln Arg Arg Ala  
 210 215 220

Arg Pro Asp Glu Arg Met Gly Arg Leu Leu Gln Gln Gly His Gly Leu  
 225 230 235 240

His Glu His Glu Gly Val Arg Gly Arg Arg His Arg Asp Arg Val Leu  
 245 250 255

Gly Ala Asp Val Glu Gly Arg Gly Arg Arg His Ala Gln Gly Gln Val  
 260 265 270

Pro Asp Gln Arg Ala Arg Pro Arg Gln Glu Glu Val Pro Asp Arg Arg  
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His Gly  
 305

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<212> DNA

<213> *Arabidopsis thaliana*

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1	5			10				15								

tca	acg	gag	caa	aca	aac	ttc	gtc	tct	cat	gta	ccg	tca	tca	ctt	tct	96
Ser	Thr	Glu	Gln	Thr	Asn	Phe	Val	Ser	His	Val	Pro	Ser	Ser	Leu	Ser	
20		25							30							

ctc	cct	caa	cga	cg	acc	tct	ctc	cga	gta	acc	gca	gcc	agg	gcc	act	144
Leu	Pro	Gln	Arg	Arg	Thr	Ser	Leu	Arg	Val	Thr	Ala	Ala	Arg	Ala	Thr	
35		40							45							

ccc	aaa	ctc	tcc	aac	cgt	aaa	ctc	cgt	gtc	gcc	gtc	atc	ggt	ggt	gga	192
Pro	Lys	Leu	Ser	Asn	Arg	Lys	Leu	Arg	Val	Ala	Val	Ile	Gly	Gly	Gly	
50		55							60							

cca	gca	ggc	gca	gct	gca	gag	act	cta	gca	caa	gga	gga	atc	gag	240
Pro	Ala	Gly	Gly	Ala	Ala	Ala	Glu	Thr	Leu	Ala	Gln	Gly	Ile	Glu	
65		70						75			80				

acg	att	ctc	atc	gag	cgt	aag	atg	gac	aat	tgc	aag	cct	tgc	ggt	ggc	288
Thr	Ile	Ile	Glu	Arg	Lys	Met	Asp	Asn	Cys	Lys	Pro	Cys	Gly	Gly		
85			90						95							

gcg	att	cct	ctc	tgt	atg	gtc	gga	gaa	ttc	aac	ttg	ccg	ttg	gat	att	336
Ala	Ile	Pro	Leu	Cys	Met	Val	Gly	Glu	Phe	Asn	Leu	Pro	Leu	Asp	Ile	
100			105							110						

att	gat	cg	aga	gtg	acg	aag	atg	aag	atg	att	tcg	ccg	tcg	aac	att	384
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Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile					
115	120	125			
gct gtt gat att ggt cgt acg ctt aag gag cat gag tat ata ggt atg					432
Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met					
130	135	140			
gtg aga aga gaa gtt ctt gat gct tat ctg aga gag aga gct gag aag					480
Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys					
145	150	155	160		
agt gga gcc act gtg att aac ggt ctc ttc ctt aag atg gat cat ccg					528
Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro					
165	170	175			
gag aat tgg gac tcg ccg tac act ttg cat tac act gag tac gat ggt					576
Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly					
180	185	190			
aaa act gga gct aca ggg acg aag aaa aca atg gag gtt gat gct gtc					624
Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val					
195	200	205			
att gga gct gat gga gct aac tct agg gtt gct aaa tct att gat gct					672
Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala					
210	215	220			
ggt gat tac gac tac gca att gca ttt cag gag agg att agg att cct					720
Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro					
225	230	235	240		
gat gag aaa atg act tac tat gag gat tta gct gag atg tat gtt gga					768
Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly					
245	250	255			
gat gat gtg tcg ccg gat ttc tat ggt tgg gtg ttc cct aag tgc gac					816
Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp					
260	265	270			
cat gta gct gtt gga aca ggt act gtg act cac aaa ggt gac atc aag					864
His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys					
275	280	285			
aag ttc cag ctc gcg acc aga aac aga gct aag gac aag att ctt gga					912
Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly					
290	295	300			
ggg aag atc atc cgt gtg gag gct cat ccg att cct gaa cat ccg aga					960
Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg					
305	310	315	320		
cca cgt agg ctc tcg aaa cgt gtg gct ctt gta ggt gat gct gca ggg					1008
Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly					
325	330	335			
tat gtg act aaa tgc tct ggt gaa ggg atc tac ttt gct gct aag agt					1056
Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser					
340	345	350			

gga aga atg tgt gct gaa gcc att gtc gaa ggt tca cag aat ggt aag	1104
Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys	
355 360 365	
aag atg att gac gaa ggg gac ttg agg aag tac ttg gag aaa tgg gat	1152
Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp	
370 375 380	
aag aca tac ttg cct acc tac agg gta ctt gat gtg ttg cag aaa gtg	1200
Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val	
385 390 395 400	
ttt tac aga tca aat ccg gct aga gaa gcg ttt gtg gag atg tgt aat	1248
Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn	
405 410 415	
gat gag tat gtt cag aag atg aca ttc gat agc tat ctg tac aag cgg	1296
Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg	
420 425 430	
gtt gcg ccg ggt agt cct ttg gag gat atc aag ttg gct gtg aac acc	1344
Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr	
435 440 445	
att gga agt ttg gtt agg gct aat gct cta agg aga gag att gag aag	1392
Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys	
450 455 460	
cct agt gtt taagaaaacaa ataatgaggt ctatctcctt tcttcatctc	1441
Leu Ser Val	
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35 40 45	
Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly	
50 55 60	
Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu	
65 70 75 80	
Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly	

85

90

95

Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile  
 100 105 110

Ile Asp Arg Arg Val Thr Lys Met Lys Met Ile Ser Pro Ser Asn Ile  
 115 120 125

Ala Val Asp Ile Gly Arg Thr Leu Lys Glu His Glu Tyr Ile Gly Met  
 130 135 140

Val Arg Arg Glu Val Leu Asp Ala Tyr Leu Arg Glu Arg Ala Glu Lys  
 145 150 155 160

Ser Gly Ala Thr Val Ile Asn Gly Leu Phe Leu Lys Met Asp His Pro  
 165 170 175

Glu Asn Trp Asp Ser Pro Tyr Thr Leu His Tyr Thr Glu Tyr Asp Gly  
 180 185 190

Lys Thr Gly Ala Thr Gly Thr Lys Lys Thr Met Glu Val Asp Ala Val  
 195 200 205

Ile Gly Ala Asp Gly Ala Asn Ser Arg Val Ala Lys Ser Ile Asp Ala  
 210 215 220

Gly Asp Tyr Asp Tyr Ala Ile Ala Phe Gln Glu Arg Ile Arg Ile Pro  
 225 230 235 240

Asp Glu Lys Met Thr Tyr Tyr Glu Asp Leu Ala Glu Met Tyr Val Gly  
 245 250 255

Asp Asp Val Ser Pro Asp Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp  
 260 265 270

His Val Ala Val Gly Thr Gly Thr Val Thr His Lys Gly Asp Ile Lys  
 275 280 285

Lys Phe Gln Leu Ala Thr Arg Asn Arg Ala Lys Asp Lys Ile Leu Gly  
 290 295 300

Gly Lys Ile Ile Arg Val Glu Ala His Pro Ile Pro Glu His Pro Arg  
 305 310 315 320

Pro Arg Arg Leu Ser Lys Arg Val Ala Leu Val Gly Asp Ala Ala Gly  
 325 330 335

Tyr Val Thr Lys Cys Ser Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser  
 340 345 350

Gly Arg Met Cys Ala Glu Ala Ile Val Glu Gly Ser Gln Asn Gly Lys  
 355 360 365

Lys Met Ile Asp Glu Gly Asp Leu Arg Lys Tyr Leu Glu Lys Trp Asp  
 370 375 380

Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val  
 385 390 395 400

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn  
 405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg  
 420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr  
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Leu Ser Val  
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21

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25

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24

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26

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